

WO 00/15838

PCT/EP99/07376

1183

SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID01

<140>

<141>

<160> 1

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:probe

<400> 1

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cctgtcaaag ataatatattt gaaatttgat caaattaatc ataaatctcc tactttgatt 180
atgggtatat tgaatatgac tcttgattca tttagtgatg gtgggaaaca ttttggaaaa 240
gaactagata atattgtgaa gcaggcagag aaattagtca gtgagggtgc tacgattatt 300
gacattggag gagtttccac acgaccagga agtggtgaac ccactgagga agaagaattg 360
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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID02

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&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

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&lt;211&gt; 2367

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;220&gt;

&lt;221&gt; CDS

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&lt;221&gt; gene

&lt;222&gt; (1)..(2364)

&lt;223&gt; Gene CaNL256

&lt;400&gt; 1

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1				5					10					15		

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Ile	Thr	Gly	Lys	Asp	Ala	Trp	Asn	Arg	Pro	Thr	Pro	Gln	Pro	Ile	Thr	
		20					25					30				

ata	tca	tta	tct	ttc	aat	act	gat	ttc	cat	aag	gca	tcg	gaa	ttg	gat	144
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gaa	ttt	atg	aaa	tca	aat	gag	cat	tta	aat	ttc	aag	tca	tta	gga	aat	240
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[illegible]

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Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe	
325	335
caa aac att tca cct ttc cag ttg ttg aaa att cta aaa gat att gaa	1056
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Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser	
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Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro	
420	430
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Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val	
435	445
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5183

Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn  
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 610 615 620

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645 650 655

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660 665 670

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675 680 685

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740 745 750

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755 760 765

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&lt;211&gt; 788

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

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1

5

10

15

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Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn  
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Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg  
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Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro  
 115 120 125

Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile  
 130 135 140

Ile Gly Val Phe Thr Phe Glu Arg Leu Gln Lys Gln Ile Val Asp Val  
 145 150 155 160

Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln  
 165 170 175

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Val Glu Ala Leu Val Ser Lys Ile Gly Gln Leu Thr Phe Gln Lys Tyr  
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Asp Gly Val Ala Glu Val Val Ala Thr Val Thr Lys Pro Asn Ala Phe  
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Ser His Val Glu Gly Val Gly Val Ser Ser Thr Met Val Lys Asp Asn  
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Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr  
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Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr  
 260 265 270

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Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly  
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Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr  
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Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe  
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Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu  
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Tyr Lys His Leu Glu Arg Lys Lys Asp Phe Asp Asn Gly Pro Arg Ser  
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Asn Leu Ile Ile Pro His Lys Ser Met Leu Glu Arg Thr Phe Val Leu  
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Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser  
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Ala Glu Ser Leu His Ser His Leu Gln Gln Leu Ile Asn Asp Lys Pro  
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Gln Glu Thr Val Gln Glu Ser Ser Asp Leu Leu Gln Phe Ile Pro Val  
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Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn  
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His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp  
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Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr  
 485 490 495

Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp  
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Ile Gly Gly Val Ser Thr Arg Pro Gly Ser Val Glu Pro Thr Glu Glu  
 515 520 525



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Glu Glu Leu Glu Arg Val Ile Pro Leu Ile Lys Ala Ile Arg Gln Ser  
 530 535 540

Leu Asn Pro Asp Leu Leu Lys Val Leu Ile Ser Val Asp Thr Tyr Arg  
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Arg Asn Val Ala Glu Gln Ser Leu Leu Val Gly Ala Asp Ile Ile Asn  
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Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala  
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Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys  
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Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile  
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Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly  
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Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val  
 755 760 765

His Asp Val Lys Glu Met Lys Asp Val Val Cys Ile Ser Asp Ala Ile  
 770 775 780

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Tyr Lys Asn Val

785

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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

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&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 647

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:probe

&lt;400&gt; 1

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aatgtgggga attggaaacc aagttatcca actcatttat ttatatttaa tgatttaatt 240
ttaattgccg ttaaaaaatc atcatctagt agtcaggaac ctactacagg gggaagtaat 300
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gcattttaata aaggtagaaa tgaaatgatt caaagtgaag gattattaga ttcaagactt 540
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ttaagaaact caggcaatta taaagaagga gttactgatg atgccggg 647
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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

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&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2373

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;220&gt;

&lt;221&gt; CDS

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&lt;222&gt; (1)..(2373)

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Asn	Arg	Lys	Ser	Arg	Ala	Val	Trp	Gln	Asn	Asn	Asn	Thr	Ser	Thr	His	
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aat	aat	cct	tat	gct	aat	tta	agc	act	ggg	gaa	aaa	agt	agg	agt	cgc	144
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ccg gca tta cct aaa ata ggt ggt gtt act act agt ggt gtt ggc ggt 432																	
Pro	Ala	Leu	Pro	Lys	Ile	Gly	Gly	Val	Thr	Thr	Ser	Gly	Val	Gly	Gly		
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			180						185					190			
aag gat aat att aat cag aat caa aaa aat att tta caa tta aca aaa 624																	
Lys	Asp	Asn	Ile	Asn	Gln	Asn	Gln	Lys	Asn	Ile	Leu	Gln	Leu	Thr	Lys		
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gac ttg aaa gag acc caa gaa gaa ttg att gaa ttg aga gga acc act 672																	
Asp	Leu	Lys	Glu	Thr	Gln	Glu	Glu	Leu	Ile	Glu	Leu	Arg	Gly	Thr	Thr		
			210					215					220				
aaa gaa tta tat gaa gtt tta ggt tat ttc aaa gaa tca gct caa cgt 720																	
Lys	Glu	Leu	Tyr	Glu	Val	Leu	Gly	Tyr	Phe	Lys	Glu	Ser	Ala	Gln	Arg		
			225					230				235			240		
aga tta gaa ttg gaa ttt gaa cca gaa aca caa aaa gaa ctt cat ctg 768																	
Arg	Leu	Glu	Leu	Glu	Phe	Glu	Pro	Glu	Thr	Gln	Lys	Glu	Leu	His	Leu		
				245						250				255			
cct caa aaa agt aat caa ttg ggt att cct agt aat aaa aag aaa gat 816																	

Pro	Gln	Lys	Ser	Asn	Gln	Leu	Gly	Ile	Pro	Ser	Asn	Lys	Lys	Lys	Asp		
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Arg	Ser	Ser	Ile	Met	Val	Leu	Lys	Lys	Met	Trp	Asp	Ser	Gln	Leu	Gln		
275								280				285					
tca	tta	ttt	aaa	cat	gtt	gac	ggg	gca	tca	aaa	ttt	gtc	caa	cca	tta	912	
Ser	Leu	Phe	Lys	His	Val	Asp	Gly	Ala	Ser	Lys	Phe	Val	Gln	Pro	Leu		
290								295				300					
ccc	aat	aga	cac	att	gtc	gcg	gaa	agt	gga	cga	tgg	ttt	gaa	gtt	aat	960	
Pro	Asn	Arg	His	Ile	Val	Ala	Glu	Ser	Gly	Arg	Trp	Phe	Glu	Val	Asn		
305								310				315				320	
gtg	ggg	aat	tgg	aaa	cca	agt	tat	cca	act	cat	tta	ttt	ata	ttt	aat	1008	
Val	Gly	Asn	Trp	Lys	Pro	Ser	Tyr	Pro	Thr	His	Leu	Phe	Ile	Phe	Asn		
325								330				335					
gat	tta	att	tta	att	act	gtt	aaa	aaa	tca	tca	tct	agt	agt	cag	gaa	1056	
Asp	Leu	Ile	Leu	Ile	Thr	Val	Lys	Lys	Ser	Ser	Ser	Ser	Ser	Gln	Glu		
340								345				350					
cct	act	aca	ggg	gga	agt	aat	ggg	ggg	tca	aaa	tcg	aga	tta	caa	gcg	1104	
Pro	Thr	Thr	Gly	Gly	Ser	Asn	Gly	Gly	Ser	Lys	Ser	Arg	Leu	Gln	Ala		
355								360				365					
gtt	caa	tgt	tgg	ccc	tta	act	caa	gta	tca	tta	caa	caa	atc	aaa	tca	1152	
Val	Gln	Cys	Trp	Pro	Leu	Thr	Gln	Val	Ser	Leu	Gln	Gln	Ile	Lys	Ser		
370								375				380					
ccg	aaa	aaa	gat	gac	gat	aag	atg	tat	ttt	atc	aat	ctt	aaa	tcc	aaa	1200	
Pro	Lys	Lys	Asp	Asp	Asp	Lys	Met	Tyr	Phe	Ile	Asn	Leu	Lys	Ser	Lys		
385								390				395				400	
tct	tta	agt	tat	gta	tac	ctg	acg	gat	cgt	tat	gat	cat	ttt	gtg	aaa	1248	
Ser	Leu	Ser	Tyr	Val	Tyr	Leu	Thr	Asp	Arg	Tyr	Asp	His	Phe	Val	Lys		
405								410				415					
gtt	acg	gaa	gca	ttt	aat	aaa	ggg	aga	aat	gaa	atg	att	caa	agt	gaa	1296	
Val	Thr	Glu	Ala	Phe	Asn	Lys	Gly	Arg	Asn	Glu	Met	Ile	Gln	Ser	Glu		
420								425				430					
aga	tta	tta	gat	tca	aga	ctt	tca	tct	cct	tca	aat	aat	aat	gga	gat	1344	
Arg	Leu	Leu	Asp	Ser	Arg	Leu	Ser	Ser	Pro	Ser	Asn	Asn	Asn	Gly	Asp		
435								440				445					
tct	aaa	gaa	gaq	aaa	cga	caa	tta	cgg	gaa	tca	tta	aga	aac	tca	ggc	1392	

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Ser	Lys	Glu	Glu	Lys	Arg	Gln	Leu	Arg	Glu	Ser	Leu	Arg	Asn	Ser	Gly	
450						455					460					
aat	tat	aaa	gaa	gga	gtt	act	gat	gat	gcc	ggg	gga	gct	gca	act	ggg	1440
Asn	Tyr	Lys	Glu	Gly	Val	Thr	Asp	Asp	Ala	Gly	Gly	Ala	Ala	Thr	Gly	
465					470					475					480	
ggg	ggg	agg	aaa	agt	gcc	ggg	act	cct	aat	aga	aat	agt	act	gat	tac	1488
Gly	Gly	Arg	Lys	Ser	Ala	Gly	Thr	Pro	Asn	Arg	Asn	Ser	Thr	Asp	Tyr	
				485					490					495		
gtt	tta	cat	gat	ata	tct	gct	cga	gta	cat	tca	cgt	aat	cga	tca	caa	1536
Val	Leu	His	Asp	Ile	Ser	Ala	Arg	Val	His	Ser	Arg	Asn	Arg	Ser	Gln	
			500					505					510			
gat	tta	ggg	aat	aat	ttc	aaa	tta	gct	aat	aat	ggg	aaa	tca	caa	ttt	1584
Asp	Leu	Gly	Asn	Asn	Phe	Lys	Leu	Ala	Asn	Asn	Gly	Lys	Ser	Gln	Phe	
			515				520					525				
ttc	aat	gaa	atc	aaa	act	tta	gaa	gat	cga	tta	gat	gat	gtt	gac	gtt	1632
Phe	Asn	Glu	Ile	Lys	Thr	Leu	Glu	Asp	Arg	Leu	Asp	Asp	Val	Asp	Val	
	530						535					540				
gaa	ata	tcg	cat	aat	caa	tat	gct	gaa	gcc	gtg	gaa	tta	ata	tca	ata	1680
Glu	Ile	Ser	His	Asn	Gln	Tyr	Ala	Glu	Ala	Val	Glu	Leu	Ile	Ser	Ile	
545					550					555					560	
att	gaa	tct	aaa	tta	cgt	aat	att	gaa	aat	gca	tta	act	aat	caa	cgt	1728
Ile	Glu	Ser	Lys	Leu	Arg	Asn	Ile	Glu	Asn	Ala	Leu	Thr	Asn	Gln	Arg	
				565					570					575		
aat	gga	ggg	aaa	aat	gtc	aat	att	gct	gat	gaa	tta	tta	ctt	tta	gat	1776
Asn	Gly	Gly	Lys	Asn	Val	Asn	Ile	Ala	Asp	Glu	Leu	Leu	Leu	Leu	Asp	
			580					585					590			
gta	tca	aaa	ttg	aaa	att	aaa	aat	cgg	aaa	gaa	aat	gta	tct	aat	gga	1824
Val	Ser	Lys	Leu	Lys	Ile	Lys	Asn	Arg	Lys	Glu	Asn	Val	Ser	Asn	Gly	
			595				600					605				
tta	ata	ttt	gat	tta	caa	cat	aat	ata	gct	aaa	ctt	aaa	caa	gat	gat	1872
Leu	Ile	Phe	Asp	Leu	Gln	His	Asn	Ile	Ala	Lys	Leu	Lys	Gln	Asp	Asp	
	610					615					620					
att	gat	aat	att	ttg	acg	tta	ttt	gat	aat	tta	gag	caa	tta	gat	cga	1920
Ile	Asp	Asn	Ile	Leu	Thr	Leu	Phe	Asp	Asn	Leu	Glu	Gln	Leu	Asp	Arg	
625					630					635					640	
ggg	gtt	caa	gga	tat	ttg	gat	tca	atg	tca	gct	tat	tta	tca	act	aca	1968

16/83

Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr	
645	650 655
gta tca aaa tta att gtt ggt tta caa gga tca acg aaa atc gat gtt	2016
Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val	
660	665 670
ggt aat tat ctt tcc aat tta atg gtt att aat gta tcg att gtg aaa	2064
Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys	
675	680 685
cgt aca att caa act tat gaa caa ata att gct cca att tta aaa cgt	2112
Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg	
690	695 700
cat ggt gat gtt gat tca agt gga ttg att aat tgg tgt att gat gaa	2160
His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu	
705	710 715 720
ttt act aaa ctt tgt aaa caa att aaa aaa cat ttg tat gga aca ttg	2208
Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu	
725	730 735
ttg ata tct tct ggg att aat atg gaa act gat gaa cca att tat aaa	2256
Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys	
740	745 750
ggt aaa gaa aga aaa tta tat gat aat ttc ttg aag att atg caa cca	2304
Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro	
755	760 765
caa ttg gaa gaa tta aaa ctg gtg gga tta aat gtt gat tat ata ttt	2352
Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe	
770	775 780
gag tct ata tta aat ctt gaa	2373
Glu Ser Ile Leu Asn Leu Glu	
785	790

&lt;210&gt; 2

&lt;211&gt; 791

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg

1

5

10

15



17/83

Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His  
 20 25 30

Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg  
 35 40 45

His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly  
 50 55 60

Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly  
 65 70 75 80

Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser  
 85 90 95

Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln  
 100 105 110

His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu  
 115 120 125

Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly  
 130 135 140

Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln  
 145 150 155 160

Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp  
 165 170 175

Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile  
 180 185 190

Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys  
 195 200 205

Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr  
 210 215 220

Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg  
 225 230 235 240

Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu  
 245 250 255

Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp  
 260 265 270

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Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln  
 275 280 285

Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu  
 290 295 300

Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn  
 305 310 315 320

Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn  
 325 330 335

Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu  
 340 345 350

Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala  
 355 360 365

Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser  
 370 375 380

Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys  
 385 390 395 400

Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys  
 405 410 415

Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu  
 420 425 430

Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp  
 435 440 445

Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly  
 450 455 460

Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly  
 465 470 475 480

Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr  
 485 490 495

Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln  
 500 505 510

Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe  
 515 520 525

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Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val  
 530 535 540

Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile  
 545 550 555 560

Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg  
 565 570 575

Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp  
 580 585 590

Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly  
 595 600 605

Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp  
 610 615 620

Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg  
 625 630 635 640

Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr  
 645 650 655

Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val  
 660 665 670

Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys  
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg  
 690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu  
 705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu  
 725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys  
 740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro  
 755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe  
 770 775 780

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Glu Ser Ile Leu Asn Leu Glu  
785 790

21/83

## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID05

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:probe

&lt;400&gt; 1

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ctgcagtaaa cctccagat ataacagact ctttatgtcc agtgatttcg ccaacaaatc 60
ttgggtgggtg ggtgtgtgtg gtccataagt atgccgtgtt gtcaccaccc ccagtcaata 120
ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180
aagtccatga attgttgga atgtcaattt cttaaagtctc atgctcatca tctaattcca 240
tctctcatc ttcttcatcg ggtggcgctt gatcatcatc tgcaacttcc tcagccactt 300
cattaacatt gatatattct tcttgagtat cgtctacgac gtc 343
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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID06

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1245)

&lt;220&gt;

&lt;221&gt; gene

&lt;222&gt; (1)..(1245)

&lt;223&gt; gene CaIR012

&lt;400&gt; 1

atg tca cac caa caa gaa gac gtc gta gac gat act caa gaa gaa tat	48
Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr	
1 5 10 15	

atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg	96
Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala	
20 25 30	

cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag	144
Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu	
35 40 45	

act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa	192
Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys	
50 55 60	

cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg	240
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His	Thr	Asp	Ser	Ile	Phe	Thr	Ile	Phe	Ser	His	Pro	Lys	Leu	Pro	Met	
65						70					75					80
gta	ttg	act	ggg	ggt	ggt	gac	aac	acg	gca	tac	tta	tgg	acc	aca	cac	288
Val	Leu	Thr	Gly	Gly	Gly	Asp	Asn	Thr	Ala	Tyr	Leu	Trp	Thr	Thr	His	
				85					90					95		
acc	caa	cca	cca	aga	ttt	gtt	ggc	gaa	atc	act	gga	cat	aaa	gag	tct	336
Thr	Gln	Pro	Pro	Arg	Phe	Val	Gly	Glu	Ile	Thr	Gly	His	Lys	Glu	Ser	
			100					105					110			
gtt	ata	tct	gga	ggg	ttt	act	gca	gac	ggc	aag	ttt	gtt	gtt	act	gca	384
Val	Ile	Ser	Gly	Gly	Phe	Thr	Ala	Asp	Gly	Lys	Phe	Val	Val	Thr	Ala	
		115					120					125				
gac	atg	aat	gga	tta	att	caa	gtt	ttc	aaa	gcc	aca	aaa	gga	ggt	gaa	432
Asp	Met	Asn	Gly	Leu	Ile	Gln	Val	Phe	Lys	Ala	Thr	Lys	Gly	Gly	Glu	
	130					135					140					
cag	tgg	gtg	aaa	ttt	ggt	gaa	ttg	gac	gaa	gtt	gaa	gaa	gtg	ttg	ttt	480
Gln	Trp	Val	Lys	Phe	Gly	Glu	Leu	Asp	Glu	Val	Glu	Glu	Val	Leu	Phe	
145					150				155						160	
gtt	act	gtg	cat	cca	aca	tta	cca	ttc	ttt	gcc	ttt	ggt	gct	acc	gat	528
Val	Thr	Val	His	Pro	Thr	Leu	Pro	Phe	Phe	Ala	Phe	Gly	Ala	Thr	Asp	
				165					170					175		
gga	tct	ata	tgg	gtc	tac	caa	ata	gac	gaa	tcc	agt	aaa	ctg	cta	gtg	576
Gly	Ser	Ile	Trp	Val	Tyr	Gln	Ile	Asp	Glu	Ser	Ser	Lys	Leu	Leu	Val	
			180					185					190			
caa	att	atg	tct	ggg	ttc	tca	cac	aca	tta	gaa	tgt	aat	ggt	gct	gta	624
Gln	Ile	Met	Ser	Gly	Phe	Ser	His	Thr	Leu	Glu	Cys	Asn	Gly	Ala	Val	
		195					200					205				
ttt	ata	caa	gga	aaa	gat	gaa	aat	gat	ttg	aca	ttg	gtc	tct	ata	agt	672
Phe	Ile	Gln	Gly	Lys	Asp	Glu	Asn	Asp	Leu	Thr	Leu	Val	Ser	Ile	Ser	
	210					215					220					
gaa	gat	ggt	act	gtg	gtg	aac	tgg	aac	tgt	ttt	aca	gga	caa	gtg	aat	720
Glu	Asp	Gly	Thr	Val	Val	Asn	Trp	Asn	Cys	Phe	Thr	Gly	Gln	Val	Asn	
225					230				235					240		
tat	aaa	ttg	caa	cct	cat	gat	gac	ttt	aaa	gga	gtt	gaa	agt	ccg	tgg	768
Tyr	Lys	Leu	Gln	Pro	His	Asp	Asp	Phe	Lys	Gly	Val	Glu	Ser	Pro	Trp	
				245				250						255		
gtc	acg	gtc	aaa	gta	cat	ggt	aat	ctt	gtg	gcc	att	ggt	ggc	aga	gat	816

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Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp  
 260 265 270

ggc cag cta tca att gtg aac aat gac act ggt aaa atc gtt cat act 864  
 Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr  
 275 280 285

ctt aaa aca ttg gat aat gtc gac gac att gca gaa ctc tca att gag 912  
 Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu  
 290 295 300

gca ttg agt tgg tgt gaa agc aaa aat att aac ctc ttg gca gtg ggt 960  
 Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly  
 305 310 315 320

ttg gtt tct ggt gac gtt tta tta ttt gat act cag caa tgg aga ttg 1008  
 Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu  
 325 330 335

aga aag aac ttg aaa gtt gac gat gcc atc acc aaa tta caa ttt gtt 1056  
 Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val  
 340 345 350

ggc gaa acc ccc att ttg gtg gga agt agt atg gat ggt aaa att tac 1104  
 Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr  
 355 360 365

aaa tgg gac gct aga act ggt gaa gag ttg ttt gct ggt gtg gga cac 1152  
 Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His  
 370 375 380

aac atg gga gta ttg gac ttt gct att tta gat gga ggt aaa aag ttg 1200  
 Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu  
 385 390 395 400

gtt act gct ggt gat gaa ggt gtt tca ttg gtc ttt gta cat gaa tag 1248  
 Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu  
 405 410 415

&lt;210&gt; 2

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr

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15



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Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala  
 20 25 30

Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu  
 35 40 45

Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys  
 50 55 60

His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met  
 65 70 75 80

Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His  
 85 90 95

Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser  
 100 105 110

Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala  
 115 120 125

Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu  
 130 135 140

Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe  
 145 150 155 160

Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp  
 165 170 175

Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val  
 180 185 190

Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val  
 195 200 205

Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser  
 210 215 220

Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn  
 225 230 235 240

Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp  
 245 250 255

Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp  
 260 265 270

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Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr  
 275 280 285

Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu  
 290 295 300

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly  
 305 310 315 320

Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu  
 325 330 335

Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val  
 340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr  
 355 360 365

Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His  
 370 375 380

Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu  
 385 390 395 400

Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu  
 405 410 415

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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID07

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 5544

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(5541)

&lt;220&gt;

&lt;221&gt; gene

&lt;222&gt; (1)..(5541)

&lt;223&gt; Gene CaJLO39

&lt;400&gt; 1

atg	agt	ggc	ata	ttt	aat	tgg	tgc	ctg	gat	gtg	ttt	gcc	gat	att	tat	48
Met	Ser	Gly	Ile	Phe	Asn	Trp	Ser	Leu	Asp	Val	Phe	Ala	Asp	Ile	Tyr	
1				5					10					15		

aac	acc	ctc	aag	ttt	gag	tcc	aat	ata	gat	ttg	gat	aca	atc	gac	ttc	96
Asn	Thr	Leu	Lys	Phe	Glu	Ser	Asn	Ile	Asp	Leu	Asp	Thr	Ile	Asp	Phe	
		20						25					30			

acc	agc	atc	aag	aat	gat	ctt	gca	aat	ggt	ttg	att	aca	cca	gtc	cct	144
Thr	Ser	Ile	Lys	Asn	Asp	Leu	Ala	Asn	Val	Leu	Ile	Thr	Pro	Val	Pro	
		35					40					45				

ctg	gat	caa	tca	cgt	agc	aaa	ctt	gga	gac	gca	tca	aaa	cca	gtg	gcg	192
Leu	Asp	Gln	Ser	Arg	Ser	Lys	Leu	Gly	Asp	Ala	Ser	Lys	Pro	Val	Ala	
		50					55				60					

ttg	ccc	agt	gga	gat	gag	gtg	aaa	ttg	aat	caa	gca	tca	att	gaa	att	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile  
 65 70 75 80

act gga gtt tta tca aat gaa ttg gat tta gat gaa cta aat aca gca 288  
 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala  
 85 90 95

gag ttg tta tat aac gca agt gac ttg agc tac aag aag gga acg tcc 336  
 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser  
 100 105 110

att ggc gat agt gct cga ttg gct tat tat tta aga gct cat tat ata 384  
 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile  
 115 120 125

cta aac att gtt gga tac tta gtt tcg cat aaa cgt tta gat atc atc 432  
 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile  
 130 135 140

act aac aac aac caa gtg ttg ttt gac aat att ttg aaa agt ttc agc 480  
 Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser  
 145 150 155 160

aag att tat act ttg agt ggt aaa tta aat gac atg att gac aag caa 528  
 Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln  
 165 170 175

aaa gtt acc ggc gac atc aac aat ctt gca ttt atc aat tgt atc aat 576  
 Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn  
 180 185 190

tat tcc aga agt cag ttg ttt aat gca cac gag tta ttg gga caa gtt 624  
 Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val  
 195 200 205

gta ttt gga tta gcg gat aat tat tat gag agt tat ggc aca cta aac 672  
 Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn  
 210 215 220

aac tat aat tcc tta gtg gag ttt ata ctg aaa aat atc agc gat gaa 720  
 Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu  
 225 230 235 240

gat gtt ttt gtt atc cat ttt tta cca tcc act tta caa ttg ttc aag 768  
 Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys  
 245 250 255

aaa tta ctt caa cta ggt gag gaa tct tta gtc gat cag ttt tac aag 816

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Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys  
 260 265 270

act ata acc tct tcc ata cta aaa gat tat gaa gcc aac aat ttt tcc 864  
 Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser  
 275 280 285

aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa 912  
 Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu  
 290 295 300

ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag 960  
 Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys  
 305 310 315 320

cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta 1008  
 Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu  
 325 330 335

aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta 1056  
 Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu  
 340 345 350

tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac 1104  
 Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp  
 355 360 365

tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca 1152  
 Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro  
 370 375 380

cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg 1200  
 Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu  
 385 390 395 400

aat gca gtt aga ccg gga tat gaa aat ata tcc aaa ttg att gac att 1248  
 Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile  
 405 410 415

tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct 1296  
 Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro  
 420 425 430

ttt ttc cag agc ttt ttc agt gtg ttt ata tct aat gcc gca gtt gtt 1344  
 Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val  
 435 440 445

atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg 1392

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Met	Thr	Ser	Leu	Arg	Asp	Ser	Glu	Glu	Asp	Phe	Val	Leu	Ser	Ser	Leu	
450						455					460					
aat	gaa	agt	gac	gaa	gag	gaa	gaa	gaa	gaa	gaa	agc	gac	agc	gac	gaa	1440
Asn	Glu	Ser	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Glu	
465					470					475					480	
gat	tct	tcg	acc	cca	aaa	aac	aaa	gaa	aaa	tca	gct	ggg	tta	gac	ctt	1488
Asp	Ser	Ser	Thr	Pro	Lys	Asn	Lys	Glu	Lys	Ser	Ala	Gly	Leu	Asp	Leu	
				485					490					495		
gac	aag	att	gcc	cag	cgt	gct	gaa	tta	gaa	agg	ttc	tac	ttg	gct	ttc	1536
Asp	Lys	Ile	Ala	Gln	Arg	Ala	Glu	Leu	Glu	Arg	Phe	Tyr	Leu	Ala	Phe	
			500					505					510			
gcg	tac	acc	tac	aac	aat	cga	cct	gaa	ttg	tgt	gcg	tta	ttt	tgg	ggg	1584
Ala	Tyr	Thr	Tyr	Asn	Asn	Arg	Pro	Glu	Leu	Cys	Ala	Leu	Phe	Trp	Gly	
		515				520					525					
aac	gag	cag	gta	act	cat	gac	att	ata	gga	ttt	att	tcc	tgg	gga	ctt	1632
Asn	Glu	Gln	Val	Thr	His	Asp	Ile	Ile	Gly	Phe	Ile	Ser	Trp	Gly	Leu	
	530					535				540						
gct	aat	aat	acg	tct	ccg	ttg	atc	act	gca	aca	ttc	tgc	tta	cta	tta	1680
Ala	Asn	Asn	Thr	Ser	Pro	Leu	Ile	Thr	Ala	Thr	Phe	Cys	Leu	Leu	Leu	
545					550					555					560	
ggg	tcg	ttg	gca	tct	gct	ggt	gca	gag	gca	act	tca	agg	ata	tgg	gag	1728
Gly	Ser	Leu	Ala	Ser	Ala	Gly	Ala	Glu	Ala	Thr	Ser	Arg	Ile	Trp	Glu	
			565					570					575			
att	ctt	gta	cac	aac	aat	aac	aac	gca	agt	acg	aga	aaa	aat	gat	ttt	1776
Ile	Leu	Val	His	Asn	Asn	Asn	Asn	Ala	Ser	Thr	Arg	Lys	Asn	Asp	Phe	
			580					585					590			
tca	aag	gta	tcc	gtt	gac	tcc	ctt	tat	gat	tcg	ttg	aaa	tat	tac	att	1824
Ser	Lys	Val	Ser	Val	Asp	Ser	Leu	Tyr	Asp	Ser	Leu	Lys	Tyr	Tyr	Ile	
		595					600					605				
gac	tct	tta	aat	gaa	agc	ttt	gaa	caa	gat	tta	aat	gcc	caa	ttg	atg	1872
Asp	Ser	Leu	Asn	Glu	Ser	Phe	Glu	Gln	Asp	Leu	Asn	Ala	Gln	Leu	Met	
		610				615						620				
ttg	aat	cag	aag	aaa	caa	gat	ttt	ctc	ttc	agc	acc	aca	aca	agc	aaa	1920
Leu	Asn	Gln	Lys	Lys	Gln	Asp	Phe	Leu	Phe	Ser	Thr	Thr	Thr	Ser	Lys	
625					630					635					640	
cag	gac	ctt	gat	gat	tct	ggc	gag	aat	aga	att	gtt	ata	gag	ttg	gcc	1968

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Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala	
645 650 655	
gag gat tca ctt gtc ctc att tca ggg ttt att caa tta ctt tct gca	2016
Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala	
660 665 670	
att gtg aag aat ttg aac act aag aat gaa aga agc aaa gaa atc aaa	2064
Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys	
675 680 685	
tcc gtg gta tac act aga ttc tca cca atc att aaa ggg ttt tta aaa	2112
Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys	
690 695 700	
ttc gat aat ttg atc aat ggt agc agg ttc ctt caa gtt gat gct agc	2160
Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser	
705 710 715 720	
att caa agc aca aac aac ccc aaa ttt att gat ttg cca aat gtt ttc	2208
Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe	
725 730 735	
gtc agt gat gac tcg aga att ata ttg acg aac ctc att cta acc ttt	2256
Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe	
740 745 750	
tta ggc gat ttt gtt acc aac gat agt gat ccg tat att aga tat gag	2304
Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu	
755 760 765	
att tgg cgt tta gtc gat cga tgg atg tac cag ggg ttg cat agt ttg	2352
Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu	
770 775 780	
cca gaa gac aag aaa gat gat gct ttt aga cat att aag aga aag tat	2400
Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr	
785 790 795 800	
aac agt aag aaa aat gtt ccc atc aat caa gca ttt tca aca aac cta	2448
Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu	
805 810 815	
act cat ctt agt caa att ggg aat ttc act gtc ttg gtg aaa aaa ttg	2496
Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu	
820 825 830	
tta acc cca tat gca gat agt aat gaa gca ttc acc aag tac tcg ttg	2544

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Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu	
835 840 845	
ttg tat cct tgt gac tta gga tta ggg tat aga ttc aac aac caa ctt	2592
Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu	
850 855 860	
gga att tgg cca tac att gaa ttt tta atg caa aat gtg ttt gca aat	2640
Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn	
865 870 875 880	
tct ggt act att gct aat aaa cga gat agg gtc aac ttg caa ctt aat	2688
Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn	
885 890 895	
ttg cta gaa tta ttt agc aat gca tta cag gga gtt gac tgg aag ttt	2736
Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe	
900 905 910	
ctt att gat gtg gca ccg aaa att att cgt gac ttg aaa aat ttt aat	2784
Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn	
915 920 925	
ggg ata ttt gac tcg ctt att cct ggt gtt caa ttg gac ttt gaa gtg	2832
Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val	
930 935 940	
ttt gtc aaa ttg cat cat tca gtt gct gtg att aac tat cta ttt gaa	2880
Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu	
945 950 955 960	
aac agg aca ttt tct gcc ttg ttt aag ctt gtt aat att gga gtt gat	2928
Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp	
965 970 975	
tct gtg aat gaa tca ggt gaa tcg gcg gaa ttg gtg tca cat gcc ctt	2976
Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu	
980 985 990	
ggg ttg att aat tct ttg ttg aga gtt caa aat tct ttt ata aac aag	3024
Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys	
995 1000 1005	
ttg tta cca ata ttg cga aac aaa gat acg cag caa caa tta cat cgt	3072
Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg	
1010 1015 1020	
ggg aca gcc att ggg att ggt act tct atg agt ctt gcg tta gca acc	3120



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Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr	1025	1030	1035	1040
cct aga acc ata ttt gat tgt ata tac tat cca aag aat ttg gga aca				3168
Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr	1045	1050	1055	
cat ggt gtt gct gat ttt tac gaa gtg ata ttg ttc cac tta tct gca				3216
His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala	1060	1065	1070	
gtt gtc caa ttt gcc ctt tat gtc agt tgt gaa aat act att tcc aac				3264
Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn	1075	1080	1085	
aaa gca att tcc ata ttg aaa gga gta agc caa tcc aag ttt ttt gtt				3312
Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val	1090	1095	1100	
acc aga gtt tca agc tct gct gat ccc tta ctc aac aac gat aga ttg				3360
Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu	1105	1110	1115	1120
att acc aca ttt gaa aac atc gac gag tca ata aaa atc aag ttt gct				3408
Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala	1125	1130	1135	
ttc att gac aag ttt gaa gaa ctc gag gac tct ttg aat atg aaa tat				3456
Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr	1140	1145	1150	
gag ata ttg gat ttt gtt ttg ggc aat ctc aat caa ttt gat ggc aaa				3504
Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys	1155	1160	1165	
gtg gct act act gcc cac ttt ttg ttg gga tac aaa gtg aaa ggc gat				3552
Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp	1170	1175	1180	
aca tta gac ttg gta cag aca aac gat caa aac aca tta cta aaa tct				3600
Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser	1185	1190	1195	1200
ttc tta aat aca ttg agc att agt ctt gat ttg att tct gaa att gat				3648
Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp	1205	1210	1215	
tac aat aat ggt aat aac cat att att gat gtt ggt cca gcc aag ctt				3696

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Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
1220	1225 1230
tcg tcg ttg att tta cag att ctt atc aag ttg tgc caa gat cca att	3744
Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
1235	1240 1245
tcg tcg tca ata aca ttg aat caa tta cgt gaa tat gaa gaa ttg ttt	3792
Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe	
1250	1255 1260
gaa aaa ttg gtt aac tgt caa cct aaa ctt gat ttg aat acc gtt tgg	3840
Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp	
1265	1270 1275 1280
tgt ggt aac cag ttt gat ggg gat ttg cag att gat gct agc aat gta	3888
Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	
1285	1290 1295
ttt gtt gac aac caa gca agc acc cag gct ttc ttt tcc ttt att aac	3936
Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn	
1300	1305 1310
cag aga aac tta att ttg cag tat ttg tca ttg gaa ttc cat agt gtc	3984
Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	
1315	1320 1325
aaa tca aga act aag cgg gag tat tat tct aaa gtg ttg acc aac gac	4032
Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	
1330	1335 1340
aag gaa ttt gtt aat cgt aca cct aag gtg ttg aca ttt tta aac att	4080
Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	
1345	1350 1355 1360
cta aat tat tca ttc aag aac ttt gaa gtg cag aaa tac gaa tgg ctt	4128
Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu	
1365	1370 1375
gac caa aaa ttt aac gtg tcg ttg tta ttg gca gaa gta aac gct caa	4176
Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln	
1380	1385 1390
aag aat ggt aca tta gat ttt tct gtt tta aca aag gtt ttc cgt ctt	4224
Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu	
1395	1400 1405
ttg tgc caa acg tca aac tta ata aca ccc gag tca aag caa ttg ttt	4272

Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe	
1410                      1415                      1420	
gcc gaa gaa att atg gtt gaa gga agt aag att tct gac ttt gtc aca	4320
Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr	
1425                      1430                      1435                      1440	
aag tac ctg gtg tcg acc gac ttg aag gat gtg cag ttg aaa tgc tta	4368
Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu	
1445                      1450                      1455	
cat tca tgg tgt caa ttg ata gag att ttg gtt act gac agt gga atc	4416
His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile	
1460                      1465                      1470	
aat tcg ctg aat ttc atc ttg gaa gtg ttg caa gtt att att ccc aaa	4464
Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys	
1475                      1480                      1485	
atc aat gac tat ttt gat gtg gac ata ctg ttt tct gaa gaa atg gtt	4512
Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val	
1490                      1495                      1500	
tca tta tgt gtt tta ttg ttt gat ctt tat gat cag ctg act ctt gcg	4560
Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala	
1505                      1510                      1515                      1520	
gac aga aaa ggt gaa gat ttt gca ctt gga att gag aga ttg atc ccc	4608
Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro	
1525                      1530                      1535	
tta ttt cag act tgt att gca ggt att ctt aat tct aac tca aca ccc	4656
Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro	
1540                      1545                      1550	
agc tta cgc tca gac ttg tat gta gtt ggc aac aag ttt ttg tta aaa	4704
Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys	
1555                      1560                      1565	
tgt ttt gag aga gag tcg ttt ttg aaa caa gtg atg cat atc atc aag	4752
Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys	
1570                      1575                      1580	
tcg gta gat aaa aag ttt ttc cag gtg att tgt aat gac gct atc tac	4800
Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr	
1585                      1590                      1595                      1600	
tca gag ggt cca tct aqa atc act tct act tta ttc ctc gag tca tta	4848

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Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu	
1605 1610 1615	
ggt cac tta ggg act ttg gtc aag gtt gat ttt att ttg aat gcg ttg	4896
Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu	
1620 1625 1630	
atc aaa aat aac gca ttg ctg ttg cta gtc agg tca gtt aag cgg act	4944
Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr	
1635 1640 1645	
gat gcc atg atc aaa ttg tgc cag gaa aaa aat tca gga gtg act tta	4992
Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu	
1650 1655 1660	
gat cat ttc ata ttt gac ttg atg gca ttc aaa gca acg cta tat ttt	5040
Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe	
1665 1670 1675 1680	
ttt gtt aga gtg gcc aaa tcg aaa aac ggg gca ttg cag ttg att caa	5088
Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln	
1685 1690 1695	
aat gaa ttg ttt tca att ttg cat cag tcg aag ttt ttg cag att gat	5136
Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp	
1700 1705 1710	
cca gat att ggt tta agt tta cga att gaa gaa gtt caa gat cac aag	5184
Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys	
1715 1720 1725	
act gtc aat gta aat gtt ttg cta gat act cca ctt tcg ata act gac	5232
Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp	
1730 1735 1740	
ttg gtg gat cca tac aag ttg cga agt gaa aac act ata tca tat ttt	5280
Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe	
1745 1750 1755 1760	
gag ttc ctt gta cca ata ttt cag cta ctt aca aca gtg tta ttg tca	5328
Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser	
1765 1770 1775	
atg gga cca aat tat caa cct gca att att caa act aga gaa ctt atg	5376
Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met	
1780 1785 1790	
aag agt gta aat cga ttg gtg gta ggt gtt atg aaa aga gat ttc ttg	5424

37183

Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu  
 1795 1800 1805

gta gag acc aaa caa att ggt caa ggg ttg tac aag gaa gag agt cac 5472  
 Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His  
 1810 1815 1820

gag ttg gta tcg ttg aaa gaa ttg gtg aag ttg ttt att ttg att gat 5520  
 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp  
 1825 1830 1835 1840

tca tta gct cat tat agt gtg tag 5544  
 Ser Leu Ala His Tyr Ser Val  
 1845

&lt;210&gt; 2

&lt;211&gt; 1847

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr  
 1 5 10 15

Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe  
 20 25 30

Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro  
 35 40 45

Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala  
 50 55 60

Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile  
 65 70 75 80

Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala  
 85 90 95

Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser  
 100 105 110

Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile  
 115 120 125

Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile  
 130 135 140

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Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser			
145	150	155	160
Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln			
	165	170	175
Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn			
	180	185	190
Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val			
	195	200	205
Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn			
	210	215	220
Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu			
225	230	235	240
Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys			
	245	250	255
Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys			
	260	265	270
Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser			
	275	280	285
Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu			
	290	295	300
Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys			
305	310	315	320
Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu			
	325	330	335
Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu			
	340	345	350
Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp			
	355	360	365
Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro			
	370	375	380
Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu			
385	390	395	400

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Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile  
 405 410 415

Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro  
 420 425 430

Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val  
 435 440 445

Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu  
 450 455 460

Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu  
 465 470 475 480

Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu  
 485 490 495

Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe  
 500 505 510

Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly  
 515 520 525

Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu  
 530 535 540

Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu  
 545 550 555 560

Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu  
 565 570 575

Ile Leu Val His Asn Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe  
 580 585 590

Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile  
 595 600 605

Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met  
 610 615 620

Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys  
 625 630 635 640

Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala  
 645 650 655

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Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala  
 660 665 670

Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys  
 675 680 685

Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys  
 690 695 700

Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser  
 705 710 715 720

Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe  
 725 730 735

Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe  
 740 745 750

Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu  
 755 760 765

Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu  
 770 775 780

Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr  
 785 790 795 800

Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu  
 805 810 815

Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu  
 820 825 830

Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu  
 835 840 845

Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu  
 850 855 860

Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn  
 865 870 875 880

Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn  
 885 890 895

Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe  
 900 905 910



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Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn  
 915 920 925

Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val  
 930 935 940

Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu  
 945 950 955 960

Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp  
 965 970 975

Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu  
 980 985 990

Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys  
 995 1000 1005

Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg  
 1010 1015 1020

Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr  
 1025 1030 1035 1040

Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr  
 1045 1050 1055

His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala  
 1060 1065 1070

Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn  
 1075 1080 1085

Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val  
 1090 1095 1100

Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu  
 1105 1110 1115 1120

Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala  
 1125 1130 1135

Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr  
 1140 1145 1150

Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys  
 1155 1160 1165

42/83

Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp  
 1170 1175 1180

Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser  
 1185 1190 1195 1200

Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp  
 1205 1210 1215

Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu  
 1220 1225 1230

Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile  
 1235 1240 1245

Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe  
 1250 1255 1260

Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp  
 1265 1270 1275 1280

Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val  
 1285 1290 1295

Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn  
 1300 1305 1310

Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val  
 1315 1320 1325

Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp  
 1330 1335 1340

Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile  
 1345 1350 1355 1360

Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu  
 1365 1370 1375

Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln  
 1380 1385 1390

Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu  
 1395 1400 1405

Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe  
 1410 1415 1420

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Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr  
 425 1430 1435 1440

Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu  
 1445 1450 1455

His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile  
 1460 1465 1470

Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys  
 1475 1480 1485

Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val  
 1490 1495 1500

Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala  
 505 1510 1515 1520

Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro  
 1525 1530 1535

Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro  
 1540 1545 1550

Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys  
 1555 1560 1565

Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys  
 1570 1575 1580

Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr  
 585 1590 1595 1600

Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu  
 1605 1610 1615

Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu  
 1620 1625 1630

Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr  
 1635 1640 1645

Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu  
 1650 1655 1660

Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe  
 665 1670 1675 1680

44/83

Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln  
1685 1690 1695

Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp  
1700 1705 1710

Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys  
1715 1720 1725

Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp  
1730 1735 1740

Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe  
745 1750 1755 1760

Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser  
1765 1770 1775

Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met  
1780 1785 1790

Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu  
1795 1800 1805

Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His  
1810 1815 1820

Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp  
825 1830 1835 1840

Ser Leu Ala His Tyr Ser Val  
1845

## SEQUENCE LISTING

45/83

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID08

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 575

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:homologous  
fragment to Sc YJL039c

&lt;400&gt; 1

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taattgcagg ttgataattt ggtcccattg acaataacac tgttgtaagt agctgaaata 120
ttggtacaag gaactcaaaa tatgatatag tgttttcact tcgcaacttg tatggatcca 180
ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240
cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaatat 360
atattntntt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420
aacaccaac ccnaaaacac ccaacacctc catcttgccc cgcttttctc tcacattttt 480
tctctactac tatcacacaa tctataaaac atacaccccc tcaaccctc ctccccaaca 540
aacctacctc cctcaactcc tatttctctc cttcc

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575

46/83  
SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID09

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 921

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(918)

<220>

<221> gene

<222> (1)..(918)

<223> Gene CaOR110

<400> 1

atg	acg	att	gaa	act	att	tat	atc	gca	aga	cac	ggt	tat	aga	tcc	aat	48
Met	Thr	Ile	Glu	Thr	Ile	Tyr	Ile	Ala	Arg	His	Gly	Tyr	Arg	Ser	Asn	
1				5					10					15		

tgg	tta	cca	cca	cca	cac	cca	cca	aat	cct	act	ggt	att	gac	agt	gac	96
Trp	Leu	Pro	Pro	Pro	His	Pro	Pro	Asn	Pro	Thr	Gly	Ile	Asp	Ser	Asp	
			20					25					30			

ccg	gct	tta	gca	cca	cat	ggt	gtt	gaa	caa	gcc	caa	cag	tta	gct	gcc	144
Pro	Ala	Leu	Ala	Pro	His	Gly	Val	Glu	Gln	Ala	Gln	Gln	Leu	Ala	Ala	
			35				40					45				

tat	ctt	aca	tca	tta	cct	aca	cat	gaa	aag	cct	gaa	ttt	att	att	gct	192
Tyr	Leu	Thr	Ser	Leu	Pro	Thr	His	Glu	Lys	Pro	Glu	Phe	Ile	Ile	Ala	
			50				55					60				

tca	cct	ttt	tat	cgt	tgt	ata	gaa	acg	tcg	aga	ccc	att	gcc	gaa	atg	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Ser	Pro	Phe	Tyr	Arg	Cys	Ile	Glu	Thr	Ser	Arg	Pro	Ile	Ala	Glu	Met	
65					70				75						80	
ttg	gac	ttg	aag	att	gct	tta	gaa	aga	gga	gtt	ggg	gaa	tgg	ttt	cgt	288
Leu	Asp	Leu	Lys	Ile	Ala	Leu	Glu	Arg	Gly	Val	Gly	Glu	Trp	Phe	Arg	
				85					90					95		
aaa	aat	aga	gat	acc	aaa	cca	gtt	ccc	ggg	gat	tac	aca	caa	ttg	aga	336
Lys	Asn	Arg	Asp	Thr	Lys	Pro	Val	Pro	Gly	Asp	Tyr	Thr	Gln	Leu	Arg	
				100					105					110		
aca	ttt	ttc	gat	aaa	tta	ttg	atc	gat	gaa	gat	act	tgg	cca	aga	gat	384
Thr	Phe	Phe	Asp	Lys	Leu	Leu	Ile	Asp	Glu	Asp	Thr	Trp	Pro	Arg	Asp	
				115					120					125		
aac	tta	aat	gtt	ata	cct	aat	att	gaa	gga	gaa	gat	tat	gat	gaa	atc	432
Asn	Leu	Asn	Val	Ile	Pro	Asn	Ile	Glu	Gly	Glu	Asp	Tyr	Asp	Glu	Ile	
				130					135					140		
tac	gat	cgt	gcc	aaa	ttg	ttt	tgg	aaa	aag	ttt	att	cct	gaa	ttt	gaa	480
Tyr	Asp	Arg	Ala	Lys	Leu	Phe	Trp	Lys	Lys	Phe	Ile	Pro	Glu	Phe	Glu	
				145					150					155		160
aag	aaa	ttc	ccc	gaa	att	aaa	aat	gtg	ttg	ata	gtt	aca	cat	gca	gca	528
Lys	Lys	Phe	Pro	Glu	Ile	Lys	Asn	Val	Leu	Ile	Val	Thr	His	Ala	Ala	
				165					170					175		
acg	aaa	att	gct	tta	gga	tca	gct	tta	tta	cag	tta	aaa	tca	gtt	act	576
Thr	Lys	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Val	Thr	
				180					185					190		
gat	gtt	ata	gat	gat	aat	caa	act	gtg	tta	cgt	gct	ggg	gca	tgt	tca	624
Asp	Val	Ile	Asp	Asp	Asn	Gln	Thr	Val	Leu	Arg	Ala	Gly	Ala	Cys	Ser	
				195					200					205		
tta	tcc	aaa	ttt	gtt	aga	gat	ggc	gaa	gat	aaa	acc	aat	cat	act	att	672
Leu	Ser	Lys	Phe	Val	Arg	Asp	Gly	Glu	Asp	Lys	Thr	Asn	His	Thr	Ile	
				210					215					220		
caa	tgg	aaa	att	gtc	atg	aat	ggg	aat	tgt	gaa	ttc	ttg	aca	cag	ggg	720
Gln	Trp	Lys	Ile	Val	Met	Asn	Gly	Asn	Cys	Glu	Phe	Leu	Thr	Gln	Gly	
				225					230					235		240
gaa	gaa	atg	aac	tgg	gat	ttc	cgt	cgt	ggg	gtt	gaa	gac	ggg	tca	gct	768
Glu	Glu	Met	Asn	Trp	Asp	Phe	Arg	Arg	Gly	Val	Glu	Ala	Gly	Ser	Ala	
				245					250					255		
gaa	gat	ata	gag	caa	aga	aag	gca	gca	gca	gaa	gca	gaa	gca	aaa	gca	816

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Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala  
 260 265 270

ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct 864  
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser  
 275 280 285

gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa gta cgt 912  
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg  
 290 295 300

aaa act tga 921  
 Lys Thr  
 305

&lt;210&gt; 2

&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn  
 1 5 10 15

Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp  
 20 25 30

Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala  
 35 40 45

Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala  
 50 55 60

Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met  
 65 70 75 80

Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg  
 85 90 95

Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg  
 100 105 110

Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp  
 115 120 125

Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile  
 130 135 140



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Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu  
 145 150 155 160

Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala  
 165 170 175

Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr  
 180 185 190

Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser  
 195 200 205

Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile  
 210 215 220

Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly  
 225 230 235 240

Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala  
 245 250 255

Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala  
 260 265 270

Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser  
 275 280 285

Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg  
 290 295 300

Lys Thr  
 305

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SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID10

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1454

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1452)

&lt;223&gt; Gene CaOR110 Splice Variant

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Splice Vaiant

&lt;400&gt; 1

atg	acg	att	gaa	act	att	tat	atc	gca	aga	cac	ggt	tat	aga	tcc	aat	48
Met	Thr	Ile	Glu	Thr	Ile	Tyr	Ile	Ala	Arg	His	Gly	Tyr	Arg	Ser	Asn	

1				5							10				15	
---	--	--	--	---	--	--	--	--	--	--	----	--	--	--	----	--

tgg	tta	cca	cca	cca	cac	cca	cca	aat	cct	act	ggt	att	gac	agt	gac	96
Trp	Leu	Pro	Pro	Pro	His	Pro	Pro	Asn	Pro	Thr	Gly	Ile	Asp	Ser	Asp	

				20							25				30	
--	--	--	--	----	--	--	--	--	--	--	----	--	--	--	----	--

ccg	gct	tta	gca	cca	cat	ggt	gtt	gaa	caa	gcc	caa	cag	tta	gct	gcc	144
Pro	Ala	Leu	Ala	Pro	His	Gly	Val	Glu	Gln	Ala	Gln	Gln	Leu	Ala	Ala	

				35											45	
--	--	--	--	----	--	--	--	--	--	--	--	--	--	--	----	--

tat	ctt	aca	tca	tta	cct	aca	cat	gaa	aag	cct	gaa	ttt	att	att	gct	192
Tyr	Leu	Thr	Ser	Leu	Pro	Thr	His	Glu	Lys	Pro	Glu	Phe	Ile	Ile	Ala	

				50											60	
--	--	--	--	----	--	--	--	--	--	--	--	--	--	--	----	--

tca	cct	ttt	tat	cgt	tgt	ata	gaa	acg	tcg	aga	ccc	att	gcc	gaa	atg	240
Ser	Pro	Phe	Tyr	Arg	Cys	Ile	Glu	Thr	Ser	Arg	Pro	Ile	Ala	Glu	Met	

5183

65	70	75	80	
ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt				288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg				
	85	90	95	
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga				336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg				
	100	105	110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat				384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp				
	115	120	125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc				432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile				
	130	135	140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa				480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu				
	145	150	155	160
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca				528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala				
	165	170	175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act				576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr				
	180	185	190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca				624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser				
	195	200	205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att				672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile				
	210	215	220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt				720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly				
	225	230	235	240
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct				768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala				
	245	250	255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca				816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala				

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260	265	270	
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Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser			
275	280	285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt			912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe			
290	295	300	
tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa			960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu			
305	310	315	320
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat			1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn			
325	330	335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat			1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp			
340	345	350	
cat cca tta gta aaa ata tcg aac aat act ata tct gct caa ggc tcg			1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser			
355	360	365	
tcg tcg tcg tcg tta tca gcg tcg aaa aat gga ttt aat agt cat act			1152
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr			
370	375	380	
cac aat tca gga gtc att gat cca tca gca ctt ata gat ggg aaa att			1200
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile			
385	390	395	400
tat cag act gat tgg aat caa tta caa ggt act gaa cta ata ttt gat			1248
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp			
405	410	415	
gaa aat ggt caa ttt ata ggc aag gtt aag gaa cat ttg act tgc aat			1296
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn			
420	425	430	
aat aac aca aaa ttc aca tta aaa aag gca gaa gaa gta gaa caa ctt			1344
Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu			
435	440	445	
cgt tca gca gat gat tct atc atg gat ata gat caa gac tca caa gga			1392
Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly			

53183

450                      455                      460  
 caa caa cca gct aga agt cag ttc tta aaa aga gca att gtg gct gct 1440  
 Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala  
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 aga gcc aaa ggt aa 1454  
 Arg Ala Lys Gly  
  
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 Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp  
             20                      25                      30  
  
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala  
             35                      40                      45  
  
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala  
             50                      55                      60  
  
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met  
     65                      70                      75                      80  
  
 Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg  
             85                      90                      95  
  
 Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg  
             100                      105                      110  
  
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp  
             115                      120                      125  
  
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile  
             130                      135                      140  
  
 Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu  
     145                      150                      155                      160  
  
 Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala

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165	170	175
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr		
180	185	190
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser		
195	200	205
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile		
210	215	220
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly		
225	230	235
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala		
245	250	255
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala		
260	265	270
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser		
275	280	285
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe		
290	295	300
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu		
305	310	315
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn		
325	330	335
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp		
340	345	350
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser		
355	360	365
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr		
370	375	380
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile		
385	390	395
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp		
405	410	415
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn		

55183

420

425

430

Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu  
435 440 445

Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly  
450 455 460

Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala  
465 470 475 480

Arg Ala Lys Gly

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SEQUENCE LISTING

<110> Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> SEQID11

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<170> PatentIn Ver. 2.1

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1 5 10 15	

cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt	96
Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser	
20 25 30	

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg	144
Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val	
35 40 45	

att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt	192
Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg	
50 55 60	

act ggt aat tta caa gtc aca tta gcc att att cag gaa tta atc aaa	240
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Thr	Gly	Asn	Leu	Gln	Val	Thr	Leu	Ala	Ile	Ile	Gln	Glu	Leu	Ile	Lys	
65					70					75					80	
aaa	tgt	agt	gaa	aac	ttg	aat	gtt	ttt	gcc	ttt	caa	gtg	tgc	tat	atc	288
Lys	Cys	Ser	Glu	Asn	Leu	Asn	Val	Phe	Ala	Phe	Gln	Val	Cys	Tyr	Ile	
				85					90					95		
ttg	caa	ctg	att	gcc	aac	act	aag	gat	ctt	gcc	ttg	tgt	aaa	aat	gtt	336
Leu	Gln	Leu	Ile	Ala	Asn	Thr	Lys	Asp	Leu	Ala	Leu	Cys	Lys	Asn	Val	
			100					105					110			
gtc	aaa	aca	ttt	ggt	gtt	ttg	tgt	gaa	aac	ttg	gat	ggt	ggg	ttg	ttc	384
Val	Lys	Thr	Phe	Gly	Val	Leu	Cys	Glu	Asn	Leu	Asp	Gly	Gly	Leu	Phe	
		115					120					125				
aca	ggt	gat	aag	gag	ttt	ata	aag	att	ttc	act	gaa	gtt	ttc	caa	aca	432
Thr	Gly	Asp	Lys	Glu	Phe	Ile	Lys	Ile	Phe	Thr	Glu	Val	Phe	Gln	Thr	
		130					135				140					
tta	gtt	tcc	ttt	ggt	aag	gac	aga	tcg	ggt	gtt	act	cag	tat	gat	tgg	480
Leu	Val	Ser	Phe	Gly	Lys	Asp	Arg	Ser	Gly	Val	Thr	Gln	Tyr	Asp	Trp	
145					150				155						160	
cag	atg	att	tct	tta	atg	gct	ata	aat	gat	ata	tcc	agt	tgt	ttg	agt	528
Gln	Met	Ile	Ser	Leu	Met	Ala	Ile	Asn	Asp	Ile	Ser	Ser	Cys	Leu	Ser	
				165					170					175		
tat	aat	gca	gct	gtt	ggt	aaa	aag	ttt	att	gct	ttg	tcg	att	cct	gtt	576
Tyr	Asn	Ala	Ala	Val	Gly	Lys	Lys	Phe	Ile	Ala	Leu	Ser	Ile	Pro	Val	
			180					185					190			
tta	ctt	cag	ttt	att	att	gca	aac	aac	cca	caa	agc	agc	ata	ttg	caa	624
Leu	Leu	Gln	Phe	Ile	Ile	Ala	Asn	Asn	Pro	Gln	Ser	Ser	Ile	Leu	Gln	
		195					200					205				
aga	ttg	aaa	tcg	aat	ctc	cac	gtt	gaa	gat	gat	ggg	aag	agg	ttg	tca	672
Arg	Leu	Lys	Ser	Asn	Leu	His	Val	Glu	Asp	Asp	Gly	Lys	Arg	Leu	Ser	
	210					215					220					
cgt	gct	cat	ctg	caa	aaa	tcc	cat	agc	aaa	att	gcc	caa	caa	att	gat	720
Arg	Ala	His	Leu	Gln	Lys	Ser	His	Ser	Lys	Ile	Ala	Gln	Gln	Ile	Asp	
225					230					235				240		
gat	gat	ttc	acc	aat	gat	tct	tta	acc	ttg	aca	gat	atc	act	gaa	aag	768
Asp	Asp	Phe	Thr	Asn	Asp	Ser	Leu	Thr	Leu	Thr	Asp	Ile	Thr	Glu	Lys	
			245					250						255		
gca	ttt	tcg	tcg	atg	aaa	tct	ttt	ttc	aat	acc	aat	gct	gcc	agt	caa	816

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Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln	
260 265 270	
atc tct gaa gtg aca aga gct gtt gtc caa cac aat att ctc aat gga	864
Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly	
275 280 285	
acc gat ttg gag tgg gga gtc tca ttc ttg gaa tta tgt att act tgg	912
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp	
290 295 300	
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Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr	
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Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met	
325 330 335	
caa ttc cag tat gct cgt tac ttg tta gga tta ctt tca tct cgt gtg	1056
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val	
340 345 350	
aac atg att ggg tta tca gtt tca gat att att caa cag ttg tta tcg	1104
Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser	
355 360 365	
ttg caa gct gat ttg att ttg aag gca agt gat ttg gac aaa agt gaa	1152
Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu	
370 375 380	
att tca att tta aca gac att tat tct gac tgt att tgt agt ttg act	1200
Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr	
385 390 395 400	
aca cat ata tat tac ttt gat caa gtc ccg gac tcg att caa gaa atc	1248
Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile	
405 410 415	
tta atc aag att gat tac att tta gaa agc agt ttt gtg gaa gat aat	1296
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn	
420 425 430	
aac att acg tcc act gga gaa caa att caa gat ttg att atc caa ttg	1344
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu	
435 440 445	
ttg gat aac att tcg aag att ttt tta att ttg aag aat aaa tca agc	1392

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Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser  
 450 455 460

tca att aat cgt aac cat gtg aat ttg gaa cat tgg gat atc agt tta 1440  
 Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu  
 465 470 475 480

gga tta ttg gct cca caa ggc gac cat gat gat aac aga aaa atg att 1488  
 Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile  
 485 490 495

att tct acg aca caa ctt atc aat atc caa gcc agg tac ttg aaa gtg 1536  
 Ile Ser Thr Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val  
 500 505 510

ttt gat gag ttt ttg aat aat gaa ttg gcg gtt ggc aat tct aaa aag 1584  
 Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys  
 515 520 525

agc tat gat ctt ctt agc aaa cag tct cgt ttg gat cct gga agt aca 1632  
 Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr  
 530 535 540

gct gtt gaa gga gtg aac aag tct gac gat ctg gac aat ggt aag gac 1680  
 Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp  
 545 550 555 560

ttt aaa aaa cct gat gcc aat caa tac att acc aat caa caa aac ttc 1728  
 Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe  
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 580 585 590

tcc ccc aac aca caa tca gtg tta ctt ttg gtt act gtt tta aaa gat 1824  
 Ser Pro Asn Thr Gln Ser Val Leu Leu Leu Val Thr Val Leu Lys Asp  
 595 600 605

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 625 630 635 640

aga cag aaa ttc aaa gat act ttt gct cat att att tta tat tac atg 1968

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Arg Gln Lys Phe Lys Asp Thr Phe Ala His Ile Ile Leu Tyr Tyr Met	
645	650 655
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Leu Lys Asp Leu Asp Glu Gln Tyr Ser His Asp Leu Gln Asn Tyr Cys	
660	665 670
aaa agc tct aaa tta ttc aaa caa ata ttg gat gct gtt gaa tat aga	2064
Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg	
675	680 685
aaa atg caa aag ttt tgg gtc cat ggc att gac cct tca cca tct gat	2112
Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp	
690	695 700
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Asn Tyr Ile Ala Ile Arg Ile Lys Pro Glu Asn Ile Glu Glu Phe Ala	
725	730 735
tgt ggt aac aac ttt ttg att gta tgg tta cat ccc caa aaa caa tta	2256
Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu	
740	745 750
ctc act gaa att gaa aaa tca caa gtc agt act cat atg agc aca ttc	2304
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755	760 765
aat aat gat tct aga aac aca aat atg aca gtg ata atg gat caa gga	2352
Asn Asn Asp Ser Arg Asn Thr Asn Met Thr Val Ile Met Asp Gln Gly	
770	775 780
tca ctg gca cta agt gga ggt gca gac cat gga ggt cac ttt gtt ccg	2400
Ser Leu Ala Leu Ser Gly Gly Ala Asp His Gly Gly His Phe Val Pro	
785	790 795 800
cca cct gaa ttt gtt aac cac acc ggt ttg tct tct gaa tct gcg tca	2448
Pro Pro Glu Phe Val Asn His Thr Gly Leu Ser Ser Glu Ser Ala Ser	
805	810 815
tca aac tca gag aaa ggt ttg tat act ggt tta gga ttg ggt act gct	2496
Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala	
820	825 830
ggt gat att act atg att cat tct gaa ata tta caa tac agt caa cat	2544

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Gly Asp Ile Thr Met Ile His Ser Glu Ile Leu Gln Tyr Ser Gln His  
 835 840 845

ttc caa gaa aga ggt tta cct cat ggt aat ggg ttt gct act att tta 2592  
 Phe Gln Glu Arg Gly Leu Pro His Gly Asn Gly Phe Ala Thr Ile Leu  
 850 855 860

cga act gtc gat agt gtt aac agt act aat gat ggg tta att tat act 2640  
 Arg Thr Val Asp Ser Val Asn Ser Thr Asn Asp Gly Leu Ile Tyr Thr  
 865 870 875 880

tat gat agt aaa tat ttg cag tca cca aga gta agt gat ttg aaa gat 2688  
 Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp  
 885 890 895

gcc atg tca aca cat agg ggt ata agg tta tct aaa cca aat ttt ggt 2736  
 Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly  
 900 905 910

ggt gcc aat gga act gct aat atg acg gat tct gct tct aca tcc aat 2784  
 Gly Ala Asn Gly Thr Ala Asn Met Thr Asp Ser Ala Ser Thr Ser Asn  
 915 920 925

gga tct gtg ttg aat aaa aat atg caa act aca gat gtt gat tca att 2832  
 Gly Ser Val Leu Asn Lys Asn Met Gln Thr Thr Asp Val Asp Ser Ile  
 930 935 940

tta agt ggt ctt gaa agt gaa gac gaa gct gcg ttt gtt gtt taa 2877  
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&lt;210&gt; 2

&lt;211&gt; 958

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

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Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser  
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Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val  
 35 40 45

Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg

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50                      55                      60  
 Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys  
 65                      70                      75                      80  
 Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile  
 85                      90                      95  
 Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val  
 100                      105                      110  
 Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe  
 115                      120                      125  
 Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr  
 130                      135                      140  
 Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp  
 145                      150                      155                      160  
 Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser  
 165                      170                      175  
 Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val  
 180                      185                      190  
 Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln  
 195                      200                      205  
 Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser  
 210                      215                      220  
 Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp  
 225                      230                      235                      240  
 Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys  
 245                      250                      255  
 Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln  
 260                      265                      270  
 Ile Ser Glu Val Thr Arg Ala Val Val Gln His Asn Ile Leu Asn Gly  
 275                      280                      285  
 Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp  
 290                      295                      300  
 Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr

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305                      310                      315                      320  
 Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met  
                          325                      330                      335  
 Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val  
                          340                      345                      350  
 Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser  
                          355                      360                      365  
 Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu  
                          370                      375                      380  
 Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr  
                          385                      390                      395                      400  
 Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile  
                          405                      410                      415  
 Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn  
                          420                      425                      430  
 Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu  
                          435                      440                      445  
 Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser  
                          450                      455                      460  
 Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu  
                          465                      470                      475                      480  
 Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile  
                          485                      490                      495  
 Ile Ser Thr Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val  
                          500                      505                      510  
 Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys  
                          515                      520                      525  
 Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr  
                          530                      535                      540  
 Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp  
                          545                      550                      555                      560  
 Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe

64183

565	570	575
Ile Ser His Phe Leu Met Tyr Ile Asp Lys Phe Phe Glu Asn Tyr Asp		
580	585	590
Ser Pro Asn Thr Gln Ser Val Leu Leu Leu Val Thr Val Leu Lys Asp		
595	600	605
Met Met Asn Ile Leu Gly Leu Asn Phe Leu Ser Asn Phe Ile Pro Phe		
610	615	620
Phe His His Trp Val Met Lys Val Asn Arg Ala Ser Asn Phe Thr Gln		
625	630	635 640
Arg Gln Lys Phe Lys Asp Thr Phe Ala His Ile Ile Leu Tyr Tyr Met		
645	650	655
Leu Lys Asp Leu Asp Glu Gln Tyr Ser His Asp Leu Gln Asn Tyr Cys		
660	665	670
Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg		
675	680	685
Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp		
690	695	700
Leu Glu Asn Thr Lys Gly Asp Arg Thr Ile Pro Thr Asp Ala Asn Gly		
705	710	715 720
Asn Tyr Ile Ala Ile Arg Ile Lys Pro Glu Asn Ile Glu Glu Phe Ala		
725	730	735
Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu		
740	745	750
Leu Thr Glu Ile Glu Lys Ser Gln Val Ser Thr His Met Ser Thr Phe		
755	760	765
Asn Asn Asp Ser Arg Asn Thr Asn Met Thr Val Ile Met Asp Gln Gly		
770	775	780
Ser Leu Ala Leu Ser Gly Gly Ala Asp His Gly Gly His Phe Val Pro		
785	790	795 800
Pro Pro Glu Phe Val Asn His Thr Gly Leu Ser Ser Glu Ser Ala Ser		
805	810	815
Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala		



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820	825	830
Gly Asp Ile Thr Met Ile His Ser Glu Ile Leu Gln Tyr Ser Gln His		
835	840	845
Phe Gln Glu Arg Gly Leu Pro His Gly Asn Gly Phe Ala Thr Ile Leu		
850	855	860
Arg Thr Val Asp Ser Val Asn Ser Thr Asn Asp Gly Leu Ile Tyr Thr		
865	870	875 880
Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp		
885	890	895
Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly		
900	905	910
Gly Ala Asn Gly Thr Ala Asn Met Thr Asp Ser Ala Ser Thr Ser Asn		
915	920	925
Gly Ser Val Leu Asn Lys Asn Met Gln Thr Thr Asp Val Asp Ser Ile		
930	935	940
Leu Ser Gly Leu Glu Ser Glu Asp Glu Ala Ala Phe Val Val		
945	950	955

66/83

## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID12

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Homologous  
fragment to Sc YMR212c

&lt;400&gt; 1

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atTTTTtacac aaggcaagat ccttagtggt ggcaatcagt tgcaagatat agcacacttg 120
aaaggcaaaa acattcaagt tttcactaca ttttttgatt aattcctgaa taatggctaa 180
tgtgacttgt aaattaccag tacggtttct accaacaatca tgatgagttt tatctttcaa 240
aaaattaatc acctttttcta atttgactct acgagtggat gcatagtata ataaataact 300
taactcggac gagttggggt ttttggtccac tgctttccca gcaggataac attgtaatat 360
taacttttga tgtttatggt gaaacaaatt cattcttgga tctggaagtt gaagaaacta 420
ttgaatcaaa acaggattta attaaccaat agaaaagaag taactcttga gttaaaaaagg 480
atattcttga tgaaaaaaag gagaaaaaag gggaaagaag actctgaaaa tgaattaaaag 540
aaacaagaaa aaagtgatca aatgattgaa taaatgaaag taggtaaaaa atga 594
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67183

## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID13

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 3771

&lt;212&gt; DNA

&lt;213&gt; Candida albicans

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(3771)

&lt;220&gt;

&lt;221&gt; gene

&lt;222&gt; (1)..(3771)

&lt;223&gt; Gene CaDR325

&lt;400&gt; 1

atg	gat	ata	cca	cca	aaa	cca	act	ctt	aag	gca	att	aag	aaa	ttt	aga	48
Met	Asp	Ile	Pro	Pro	Lys	Pro	Thr	Leu	Lys	Ala	Ile	Lys	Lys	Phe	Arg	
1				5					10					15		

act	ttg	gat	gaa	ata	aaa	tat	gcc	atg	aaa	cat	gtt	ttc	caa	gat	gct	96
Thr	Leu	Asp	Glu	Ile	Lys	Tyr	Ala	Met	Lys	His	Val	Phe	Gln	Asp	Ala	
			20					25					30			

caa	tta	ggt	tta	gca	gga	cat	aga	aaa	tta	gtg	gta	att	ttg	aaa	aat	144
Gln	Leu	Gly	Leu	Ala	Gly	His	Arg	Lys	Leu	Val	Val	Ile	Leu	Lys	Asn	
			35				40						45			

gta	ttt	aaa	aaa	gcc	att	gaa	tta	aat	caa	att	aat	ttc	ttt	gcc	atg	192
Val	Phe	Lys	Lys	Ala	Ile	Glu	Leu	Asn	Gln	Ile	Asn	Phe	Phe	Ala	Met	
			50				55						60			

tgt	ttt	act	aaa	ttg	tta	tct	aaa	gta	tta	cct	ttg	aaa	aga	gga	gtt	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val  
 65 70 75 80  
 ttg gca ggt gat aga ata gtc aaa ttt tgt tat ctg ttt gtt aat ggt 288  
 Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly  
 85 90 95  
 ctt gta aaa gat gcc aat gaa gaa aaa cgt tcc aaa gaa gaa gaa aaa 336  
 Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys  
 100 105 110  
 gaa gaa aaa gac aaa gac gaa gac aaa gat acg aat gaa agt gat aaa 384  
 Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys  
 115 120 125  
 aat gaa gaa gat cag gaa gat caa gaa gga gaa gga gat caa gaa act 432  
 Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr  
 130 135 140  
 cca att tcg gaa ttc ata tca tat ttg ata aaa tat tta ttg agt ggg 480  
 Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly  
 145 150 155 160  
 ata gag gct aaa gat aaa ctg gtt cgt tat cgt gtt gta caa aca tta 528  
 Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu  
 165 170 175  
 gca tac ttg gtt gaa ttc ttg acc gag ata cac gag aat aat aca ttg 576  
 Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu  
 180 185 190  
 gaa gcg tta tat act tta tta agt aat agg cta caa gat aaa gag ctg 624  
 Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu  
 195 200 205  
 tcg ata cgt att caa gct gtt gtg gca tta tca cat ttt caa tta ttt 672  
 Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe  
 210 215 220  
 gaa ttt agt att gaa ggt gat act gga gaa ttt gag gat gaa tta ata 720  
 Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile  
 225 230 235 240  
 tca agt aac caa att cag aat aaa ttg ata aat tcc att caa aat gat 768  
 Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp  
 245 250 255  
 gat agt cca gaa gtc aga cgt gca gca tta atg aat ttg gtt aaa aca 816

63183

Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr  
 260 265 270

caa gat aca ata ccg att tta ctt gaa cga gcc aga gat tcc aat tct 864  
 Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser  
 275 280 285

att aat aga aga ttg gtt tat tct aaa ata gct cgt gaa tta ata act 912  
 Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr  
 290 295 300

gat ttg gat gat ctt gaa ttt gaa gat agg gaa ttt tta tta aaa tgg 960  
 Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp  
 305 310 315 320

ggg tta aat gat cgt gat gaa act gtt aaa gca gcc gcc act aaa atg 1008  
 Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met  
 325 330 335

ctt acc att tat tgg tat caa tct gtc aat gaa gat tta tta gaa tta 1056  
 Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu  
 340 345 350

att gat caa tta aat gtc aag agt gct ata gct gaa cag gcc ata tta 1104  
 Ile Asp Gln Leu Asn Val Lys Ser Ala Ile Ala Glu Gln Ala Ile Leu  
 355 360 365

gca ttt ttt aaa aat aaa cca gaa gtt ctt gaa act att aaa att gat 1152  
 Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp  
 370 375 380

gaa tca tat tgg aaa aat cta act aca gaa aag gca ttc ttg atg agg 1200  
 Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg  
 385 390 395 400

acg ttt tat caa tat tgt aat gag aat caa tta cat gct tta atg gat 1248  
 Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp  
 405 410 415

gcc aat ttc cct gaa tta ctt gat ttg tca ata aca tta gaa aag tat 1296  
 Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr  
 420 425 430

ttg tca gtg agg ttg aaa act ata aat gaa aat gaa aat tta gtt aag 1344  
 Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys  
 435 440 445

aca tgg gaa act tat aat gcc aag att gac gaa tta gat gat caa ata 1392

70183

Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile  
 450 455 460

ttt agt ctt gaa aac cag att tcc aga ata aat act gat gcc gat aat 1440  
 Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn  
 465 470 475 480

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 Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn  
 485 490 495

att gct aag gat ttg ttc aaa aag aga att aaa caa ttg aaa aac aac 1536  
 Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn  
 500 505 510

agt ggg aat cta gaa gat ttg att act gaa gaa aat caa gag att gct 1584  
 Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala  
 515 520 525

gat caa atc aag gat ttc ctg atg gaa gat ttg caa caa caa ttg gaa 1632  
 Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu  
 530 535 540

gat atc aat aaa aat ctt gat gaa att gaa cat cat cca gaa gat ata 1680  
 Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile  
 545 550 555 560

acg gct aaa tta gaa gaa ctt caa aca aaa tat gat tct tgt att agg 1728  
 Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg  
 565 570 575

gcg ctt gaa acc act agt gaa ttg aaa att cag act gtt caa atc ttt 1776  
 Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe  
 580 585 590

gaa caa gaa cat gaa aat gat tgt atc ccc ttt gta gat gct ttg aaa 1824  
 Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys  
 595 600 605

gaa tta gaa ttc att att aat caa tta tta tta att gtt aaa gat ttt 1872  
 Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe  
 610 615 620

gat tat gga gat gaa atg gca aga aga aaa ttg tta cat ata ata aga 1920  
 Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg  
 625 630 635 640

atg aca tta act gaa gat aaa tta cct gat gcg tta ata tca gtg gca 1968

71183

Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala  
645 650 655

ctt aga gta tta cga gca ctt tct ata aat gaa aaa gat ttt gtt tcc 2016  
Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser  
660 665 670

atg gcg gta gaa ata att act gat att cgt gat tct cga gat gat gaa 2064  
Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu  
675 680 685

gag ttc cat tct gct gcc gct aca ttt gat gat gat gat gat gat att 2112  
Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Asp Ile  
690 695 700

ttg gga aat ggt gat gat gaa tct caa caa tca tca tca ctc agt gca 2160  
Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala  
705 710 715 720

gta aca aag aag cga aga att gaa cca gat atg cca cca gat gat att 2208  
Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile  
725 730 735

gtg tta aga tgt ctt acc atg aca caa tat gta ttg gaa gta att act 2256  
Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr  
740 745 750

cat agt ttg gat gat cat ctt tca ttg agt tct att tac agt ggt att 2304  
His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile  
755 760 765

gtc aat tat gct att cag aat gaa tcg aaa aag aaa tta tat ctt gct 2352  
Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala  
770 775 780

ggg tta act tgt tta gga ctt tat tct tta att gat tcc aaa att gcc 2400  
Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala  
785 790 795 800

aga att gca act aca aca tta tta ctg gca atg aga agt aat ggt gaa 2448  
Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu  
805 810 815

gaa gtg aaa gag att gga atg aaa gct att gtg gat ata ttg gca att 2496  
Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile  
820 825 830

tat ggt atg agt att ctt gat aaa tca tct aaa tac aaa tat tca aga 2544

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Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg  
 835 840 845

atg ttt ttc aaa gtt tta aat tca ttt gat gca cca aaa tta caa tgc 2592  
 Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys  
 850 855 860

att gtc gct gaa gga tta tgc aaa ttg ttt tta gcc gat att ttg tac 2640  
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 865 870 875 880

aag act gac aaa cgg agt tta ttt gga aat gct att caa ggt ggt ggt 2688  
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 885 890 895

ggt ggt ggt ggt ggt aat gat gat cca act acc acc aat gac gat gaa 2736  
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 900 905 910

act gaa gaa gaa aca gat cga gag cat gaa aag cat tta ttt gaa gcg 2784  
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 915 920 925

att gta ctt att tat ttc aac ccc aac acc aaa tca aat caa gaa tta 2832  
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 930 935 940

caa caa att ttg tca ttt tgt att cca gtt tat gcc ttt tct cat ata 2880  
 Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile  
 945 950 955 960

aat cat caa atc aat tta gct gca gtt agt ggt gat gtt att tat cga 2928  
 Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg  
 965 970 975

ctt ttc act gaa aca gaa aca gaa tta tca cca agt gtt ata atc cct 2976  
 Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro  
 980 985 990

caa tta ata tca tgg tgt gat cct cga aat tta gtt aaa tta tgc aat 3024  
 Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn  
 995 1000 1005

gag gaa ata aat caa gca aca tca cat tta tgg caa tgt gtt tat tta 3072  
 Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu  
 1010 1015 1020

tta caa gtg gtt gaa caa gta gat gct cgt aat gtt aaa aga tgc atc 3120



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Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile  
 1025 1030 1035 1040

att aac aat ttg aat aaa ttt cat ata acg gaa gaa tta gag tca aat 3168  
 Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn  
 1045 1050 1055

caa tta caa gct tta att aaa gct ctt gat gct aca gtt gaa tta ttt 3216  
 Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe  
 1060 1065 1070

act aat aat gaa gat aac cct aat ttt atc ttg gat aaa cca aca aag 3264  
 Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys  
 1075 1080 1085

aag aat ttt gat act ttt att gaa tca ata aag aat aaa ttg gaa att 3312  
 Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile  
 1090 1095 1100

gct caa aaa aga gaa gaa aat gaa ctg att aaa agt ggt aca aat tca 3360  
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 1105 1110 1115 1120

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 Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser  
 1125 1130 1135

caa ata tct ata aaa tca gaa aca aaa aga aga gat ctg gat cga tct 3456  
 Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser  
 1140 1145 1150

ctg caa gtt agt aaa act acg tca cca gaa act tca gaa aat gaa gat 3504  
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 1155 1160 1165

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 Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe  
 1170 1175 1180

act gat gga aaa aat aaa ctt gaa cta aag gca gat aag cca atc aca 3600  
 Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr  
 1185 1190 1195 1200

ttt aaa gct gaa gac aag agg gaa ggg tca gtt gaa aca gat cat ggt 3648  
 Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly  
 1205 1210 1215

caa gaa caa gtt cta gtt gaa tca aag aaa gtc att gat agt aat gtt 3696

74183

Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val  
 1220 1225 1230

gaa gat tct tta gaa gat ata gat aag ttt tta gaa gaa gca gat gat 3744  
 Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp  
 1235 1240 1245

gtt gat tat ggt gat att tca atg gat 3771  
 Val Asp Tyr Gly Asp Ile Ser Met Asp  
 1250 1255

&lt;210&gt; 2

&lt;211&gt; 1257

&lt;212&gt; PRT

&lt;213&gt; Candida albicans

&lt;400&gt; 2

Met Asp Ile Pro Pro Lys Pro Thr Leu Lys Ala Ile Lys Lys Phe Arg  
 1 5 10 15

Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala  
 20 25 30

Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn  
 35 40 45

Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met  
 50 55 60

Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val  
 65 70 75 80

Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly  
 85 90 95

Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys  
 100 105 110

Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys  
 115 120 125

Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr  
 130 135 140

Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly  
 145 150 155 160

75183

Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu  
 165 170 175

Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu  
 180 185 190

Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu  
 195 200 205

Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe  
 210 215 220

Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile  
 225 230 235 240

Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp  
 245 250 255

Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr  
 260 265 270

Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser  
 275 280 285

Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr  
 290 295 300

Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp  
 305 310 315 320

Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met  
 325 330 335

Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu  
 340 345 350

Ile Asp Gln Leu Asn Val Lys Ser Ala Ile Ala Glu Gln Ala Ile Leu  
 355 360 365

Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp  
 370 375 380

Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg  
 385 390 395 400

Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp  
 405 410 415

76183

Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr  
 420 425 430

Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys  
 435 440 445

Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile  
 450 455 460

Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn  
 465 470 475 480

Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn  
 485 490 495

Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn  
 500 505 510

Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala  
 515 520 525

Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu  
 530 535 540

Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile  
 545 550 555 560

Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg  
 565 570 575

Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe  
 580 585 590

Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys  
 595 600 605

Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe  
 610 615 620

Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg  
 625 630 635 640

Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala  
 645 650 655

Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser  
 660 665 670

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Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu  
675 680 685

Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Ile  
690 695 700

Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala  
705 710 715 720

Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile  
725 730 735

Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr  
740 745 750

His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile  
755 760 765

Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala  
770 775 780

Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala  
785 790 795 800

Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu  
805 810 815

Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile  
820 825 830

Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg  
835 840 845

Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys  
850 855 860

Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr  
865 870 875 880

Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly  
885 890 895

Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu  
900 905 910

Thr Glu Glu Glu Thr Asp Arg Glu His Glu Lys His Leu Phe Glu Ala  
915 920 925

78183

Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu  
 930 935 940

Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile  
 945 950 955 960

Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg  
 965 970 975

Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro  
 980 985 990

Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn  
 995 1000 1005

Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu  
 1010 1015 1020

Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile  
 1025 1030 1035 1040

Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn  
 1045 1050 1055

Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe  
 1060 1065 1070

Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys  
 1075 1080 1085

Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile  
 1090 1095 1100

Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser  
 1105 1110 1115 1120

Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser  
 1125 1130 1135

Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser  
 1140 1145 1150

Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp  
 1155 1160 1165

Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe  
 1170 1175 1180

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Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr  
185 1190 1195 1200

Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly  
1205 1210 1215

Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val  
1220 1225 1230

Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp  
1235 1240 1245

Val Asp Tyr Gly Asp Ile Ser Met Asp  
1250 1255

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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID14

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Homologous  
fragment to Sc YDR325

&lt;400&gt; 1

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ctgtttgtta atggtcttgt aaaagatgcc aatgaagaaa aacgttccaa agaagaagaa 60
aaagaagaga aagacaaaga caaagacaaa gatacgaatg aaagtgataa aaatgaagaa 120
gatacaggaag atcaagaagg agaaggagat caagaaactc caatttcgga attcatatca 180
tatttgataa aatatttatt gagtgggata gaggctaaaag ataaactggt tcgttatcgt 240
gttgtaaaaa cattagcata cttggttgaa ttcttgaccg agatacacga gaataatata 300
ttggaagcgt tatatacttt attaagtaat aggctacaag ataaagagct gtcgatacgt 360
attcaagctg ttgtggcatt atcacatttt caattatttg aatttagtat tgaaggatgat 420
actggagaat ttgaggatga attaatatca agtaacccaa ttcagaataa attgataaat 480
tccattcaaa atgatgatag tccagaagtc agacgtgcag cattaatgaa tttgggttaa 540
acacaagata caataccgat tttacttgag cgagccagag attccaattc tattaataga 600
aga 603
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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES.

&lt;130&gt; SEQID15

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Homologous  
fragment to Sc YDR325

&lt;400&gt; 1

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gggggttaa at gatcgtgatg aatctgttaa agcagccgcc tttaaaatgc taaccattta 60
ttggtatcaa tctgtcaatg aagattttatt agaattaatt gatcaattaa atgtcagaag 120
tgctatagct gaacaggcca tattagcatt ttttaaaaaat aaaccagaag ttcttgcaac 180
tattaaaatt gatgaatcat attggaaaaa tctaactaca gaaaaggcat tcttgatgag 240
gacgttttat caatattgta atgagaatca attacatgct ttaatggatg ccaatttccc 300
tgaattactt gatttgtcaa taacattaga aaagtatttg tcagtggagt tgaaaacaat 360
aaatgaaaat gaaaatttaa ttaagacatg ggaaacttat aatgccaaga ttgacgaatt 420
agatgatcaa atatttagtc ttgaaaacca gatttccaga ataaatactg atgccgataa 480
tttccgtaaa agtttatcta acattgaaga agatattatt gaaatcaata ttgctaagga 540
tttgttcaaa aagagaatta aacaattgaa aaactgagca c 581
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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID16

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Homologous  
fragment to Sc YDR325

&lt;400&gt; 1

```
tggtgactca attcatttga tgcacaaaaa ttacaatgca ttgtcgctga gtagattatg 60
caaattgttt ttagccgata ttttgtacaa gactgacaaa cggatttatt tggaaatgct 120
attcaagggtg gtggtggtgg tgatgatcca actaccacca atgacgatga aactgaagaa 180
gaaacagatc gagagcatga aaagcattta tttgaagcga ttgtacttat ttatttcaac 240
cccaacacca aatcaaatca agaattacaa caaattttgt cattttgtat tccagtttat 300
gcctttttctc atataaatca tcaaatcaat ttagctgcag ttagtggtga tgttatttat 360
cgacttttca ctgaaacaga aacagaatta tcaccaagtg ttataatccc tcaattaata 420
tcattggtgtg atcctcgaaa tttagttaaa ttatcgaatg aggaaataaa tcaagcaaca 480
tcacatttat ggcaatgtgt ttatttatta caagtgggtg aacaagtaga tgctcgtaat 540
gttaaaagat gcatcattaa caatttgaat aaatttcata taacggaaga attagaatca 600
aatcaattac aagctttaat taaagctctt gatgctacag ttgaattatt tactaataat 660
ga
```

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## SEQUENCE LISTING

&lt;110&gt; Hoechst Marion Roussel

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR  
SCREENING SUBSTANCES USING SAID GENES

&lt;130&gt; SEQID17

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 1

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:Homologous  
fragment to Sc YOR110

&lt;400&gt; 1

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atattgtgttg atagttacac atgcagcaac gaaaattgct ttaggatcag ctttattaca 60
gttaaaatca gttactgatg ttatagatga taatcaaact gtgttacgtg ctggtgcatg 120
ttcattatcc aaatttggtta gagatggcga agataaaacc aatcatacta ttcaatggaa 180
aattgtcatg aatggtaatt gtgaattctt gacacagggt gaagaaatga a          231
```